

Figure 1 (SEQ ID NO:724)

85P1B3 SSH sequence and GenBank homology to OIP5

GATCAGAGGACACATGGGACTCTGCATCTTAATTCCTAAATTTACAGTCAAAGACATTTTCAG
 AGATAAGTATTATGAATTCAATAAGAATCTAAAGTAAGTTCTTAAGGCAAATAGCTATAAAA
 GAGAAGAATCCTTAGTCTCTCATCTTCTAAAAACAGCTTCACAAATAATTTGGAAAATCAGCC
 TAAAGGTAAATAGAACTGCATTTCCCCTCCATTCTTGAAGCCAATCTTTTCAAGAAATGAC
 TAAGCAGCACCTGTTGTTGAAGACAGCAATAAAGCCTGAACCTGACACTCAAGCTTTGGTACA
 GGATC

gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein... 632 e-179
 gb|AF158642.1|AF158642 Homo sapiens metalloproteinase-disin... 42 0.12
 gb|AC005075.2|AC005075 Homo sapiens clone RG219E16, complet... 42 0.12
 emb|AL096773.6|HS1000E10 Human DNA sequence from clone 1000... 40 0.48

>gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein OIP5 mRNA, partial cds
 Length = 1197

Score = 632 bits (319), Expect = e-179
 Identities = 319/319 (100%)
 Strand = Plus / Minus

Query: 1 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacatttt 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1013 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacatttt 954

Query: 61 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatagcta 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 953 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatagcta 894

Query: 121 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgaa 180
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 Sbjct: 893 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgaa 834

Query: 181 aatcagcctaaaggtaaatagaactgcatttcccctccattcttgaagccaatcttttt 240
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 Sbjct: 833 aatcagcctaaaggtaaatagaactgcatttcccctccattcttgaagccaatcttttt 774

Query: 241 caagaaatgactaagcagcacctgttggtgaagacagcaataaagcctgaacctgacact 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 773 caagaaatgactaagcagcacctgttggtgaagacagcaataaagcctgaacctgacact 714

Query: 301 caagctttggtacaggatc 319 (SEQ ID NO:725)
 ||||||||||||||||
 Sbjct: 713 caagctttggtacaggatc 695 (SEQ ID NO:726)

Figure 2

cDNA Sequence and ORF of 85P1B3/OIP5 clone A
(SEQ ID NO:727)

```

5'   9      18      27      36      45      54
    GGC TGC GGG AAG ATG GCG GCT CAG CCG CTG CGG CAT CGC TCA CGT TGT GCA ACG
    -----
    (SEQ ID NO:728)→ M  A  A  Q  P  L  R  H  R  S  R  C  A  T

    63      72      81      90      99      108
    CCG CCC CGG GGG GAC TTT TGT GGT GGC ACT GAG AGG GCG ATT GAC CAA GCT TCT
    -----
    P  P  R  G  D  F  C  G  G  T  E  R  A  I  D  Q  A  S

    117     126     135     144     153     162
    TTT ACG ACC TCC ATG GAG TGG GAT ACG CAG GTG GTG AAG GGG TCC TCG CCG CTC
    -----
    F  T  T  S  M  E  W  D  T  Q  V  V  K  G  S  S  P  L

    171     180     189     198     207     216
    GGC CCC GCA GGG CTG GGG GCT GAG GAG CCA GCC GCC GGC CCG CAG CTG CCG TCT
    -----
    G  P  A  G  L  G  A  E  E  P  A  A  G  P  Q  L  P  S

    225     234     243     252     261     270
    TGG CTG CAG CCT GAG AGG TGC GCT GTG TTC CAG TGC GCA CAG TGT CAC GCA GTG
    -----
    W  L  Q  P  E  R  C  A  V  F  Q  C  A  Q  C  H  A  V

    279     288     297     306     315     324
    CTC GCC GAC TCG GTG CAC CTC GCC TGG GAC CTG TCG CGG TCC CTC GGG GCC GTG
    -----
    L  A  D  S  V  H  L  A  W  D  L  S  R  S  L  G  A  V

    333     342     351     360     369     378
    GTC TTC TCC AGA GTT ACA AAT AAC GTC GTT TTG GAA GCG CCC TTC CTA GTT GGC
    -----
    V  F  S  R  V  T  N  N  V  V  L  E  A  P  F  L  V  G

    387     396     405     414     423     432
    ATT GAA GGT TCA CTC AAA GGC AGT ACT TAC AAC CTT TTA TTC TGT GGT TCT TGT
    -----
    I  E  G  S  L  K  G  S  T  Y  N  L  L  F  C  G  S  C

    441     450     459     468     477     486
    GGG ATT CCC GTT GGT TTC CAT CTG TAT TCT ACC CAT GCT GCC CTG GCT GCC TTG
    -----
    G  I  P  V  G  F  H  L  Y  S  T  H  A  A  L  A  A  L

    495     504     513     522     531     540
    AGA GGT CAC TTC TGC CTT TCC AGT GAC AAA ATG GTG TGC TAT CTC TTA AAA ACA
    -----
    R  G  H  F  C  L  S  S  D  K  M  V  C  Y  L  L  K  T

    549     558     567     576     585     594
    AAA GCC ATA GTA AAT GCA TCA GAG ATG GAT ATT CAA AAT GTT CCT CTA TCA GAA
    -----
    K  A  I  V  N  A  S  E  M  D  I  Q  N  V  P  L  S  E

    603     612     621     630     639     648
    AAG ATT GCA GAG CTG AAA GAG AAG ATA GTG CTA ACG CAC AAT CGC TTA AAA TCA
    -----
    K  I  A  E  L  K  E  K  I  V  L  T  H  N  R  L  K  S
  
```

Sheet 3 of 22

CTA	ATG	AAG	ATT	CTG	AGT	GAA	GTG	ACT	CCT	GAC	CAG	TCC	AAG	CCA	GAA	AAC	TGA
L	M	K	I	L	S	E	V	T	P	D	Q	S	K	P	E	N	*
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85P1B3/OIP5 protein sequence. (SEQ ID NO:729)

1 MAAQPLRHRS RCATPPRGDF CGGTERAIDQ ASFTTSMEDW TQVVKGSSPL GPAGLGAEPP
61 AAGPQLPSWL QPERCAVFQC AQCHAVLADS VHLAWDLRS LGAVVFSRVT NNVVLEAPFL
121 VGIEGSLKGS TYNLLFCGSC GIPVGFHLYS THAALAALRG HFCLSSDKMV CYLLKTKAIV
181 NASEMDIQNV PLSEKIAELK EKIVLTHNRL KSLMKILSEV TPDQSKPEN*

Figure 4

Alignment of 85P1B3 with OIP5.

>gi|2815610|gb|AAC39561.1| (AF025441) Opa-interacting protein OIP5 [Homo sapiens]
Length = 231

Score = 462 bits (1189), Expect = e-130

Identities = 229/229 (100%), Positives = 229/229 (100%)

```
85P1B3: 1  MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEPP 60
      MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEPP
OIP5: 3  MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEPP 62

85P1B3: 61  AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTTNNVVLEAPFL 120
      AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTTNNVVLEAPFL
OIP5: 63  AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTTNNVVLEAPFL 122

85P1B3:121  VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 180
      VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV
OIP5: 123  VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV 182

85P1B3:181  NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 229 (SEQ ID NO:730)
      NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN
OIP5: 183  NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 231 (SEQ ID NO:731)
```

Figure 5: 85P1B3 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

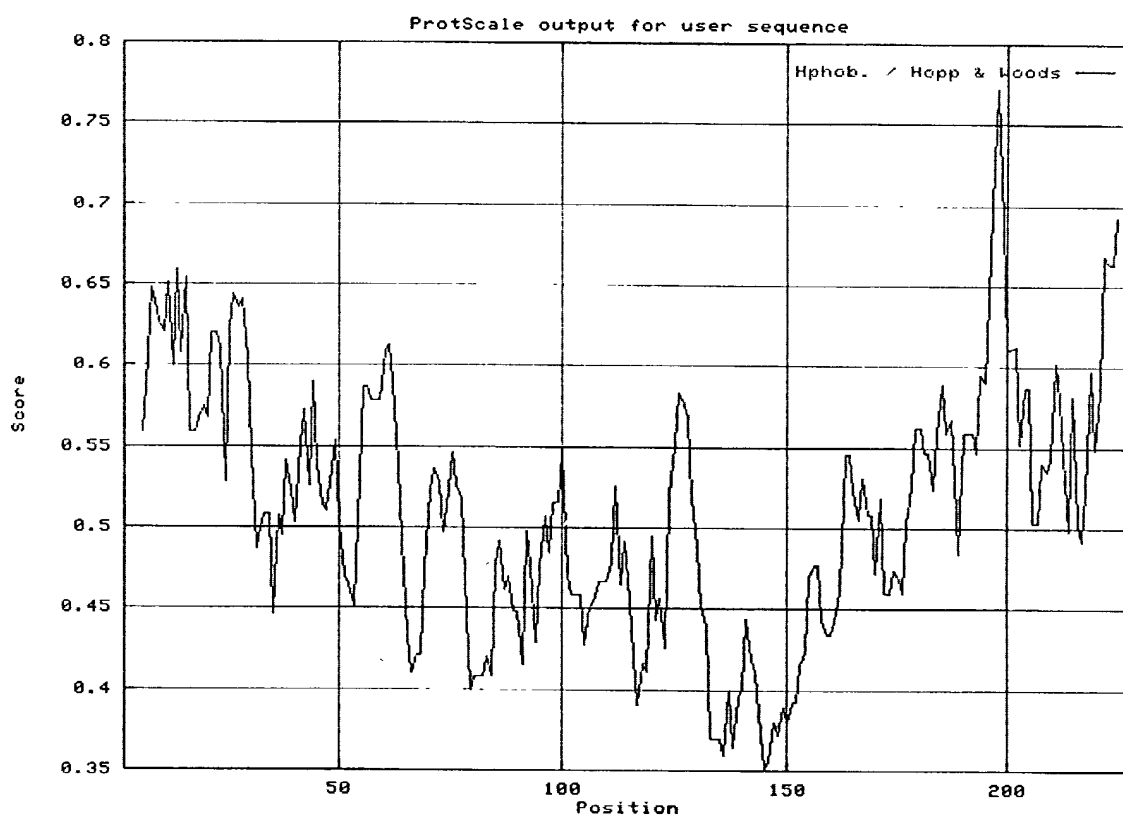


Figure 6: 85P1B3 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

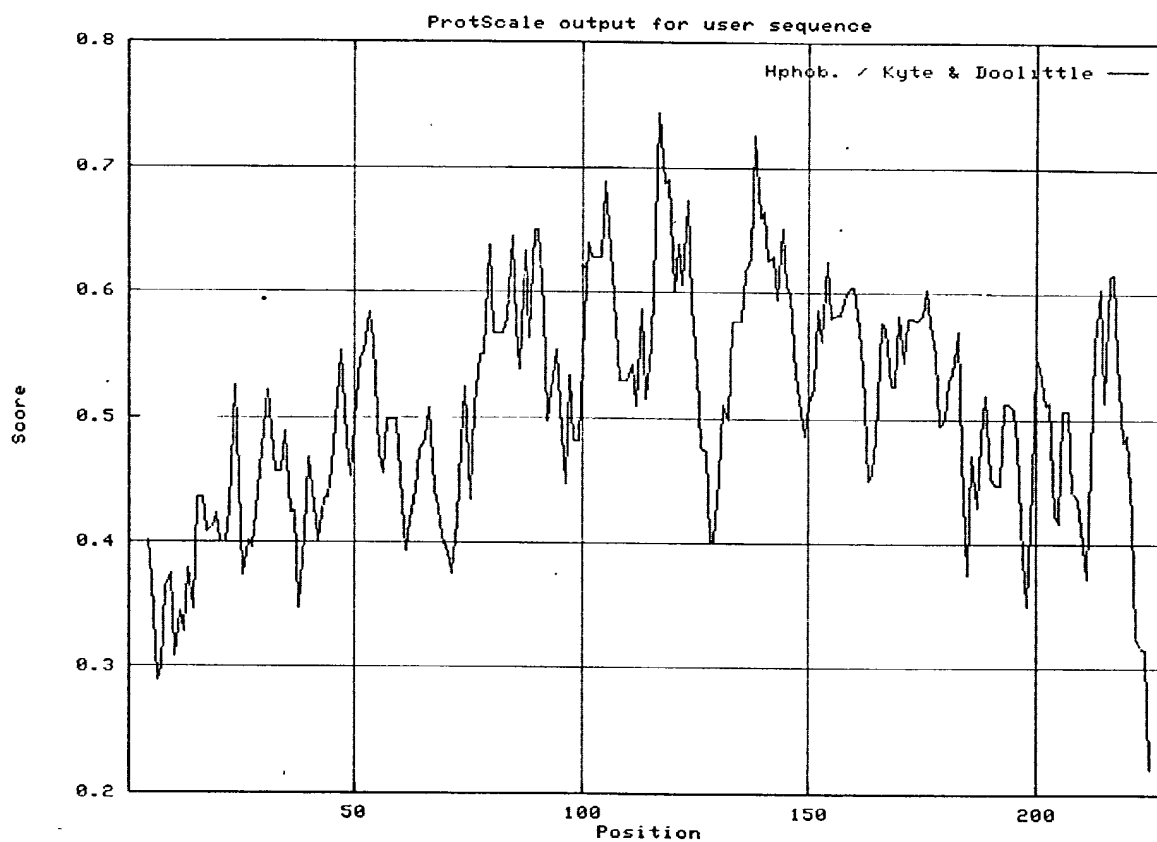


Figure 7: 85P1B3 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

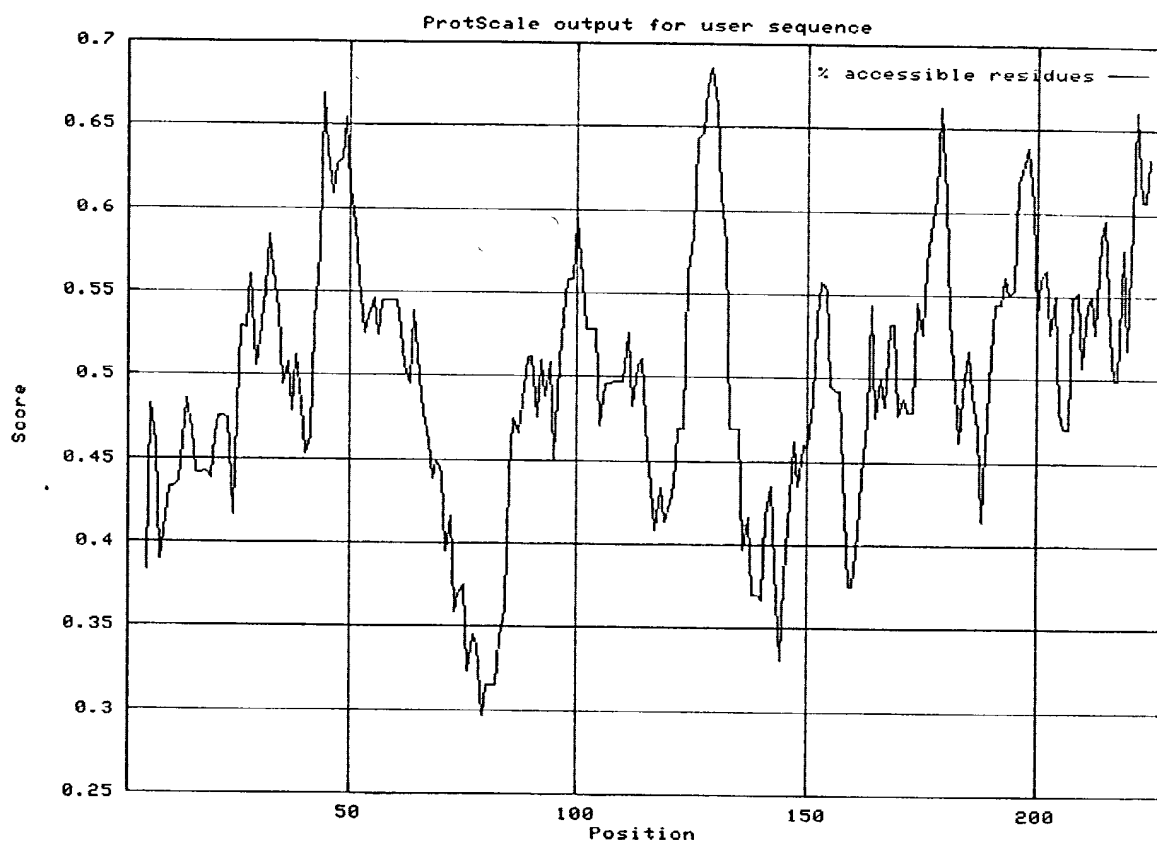


Figure 8: 85P1B3 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

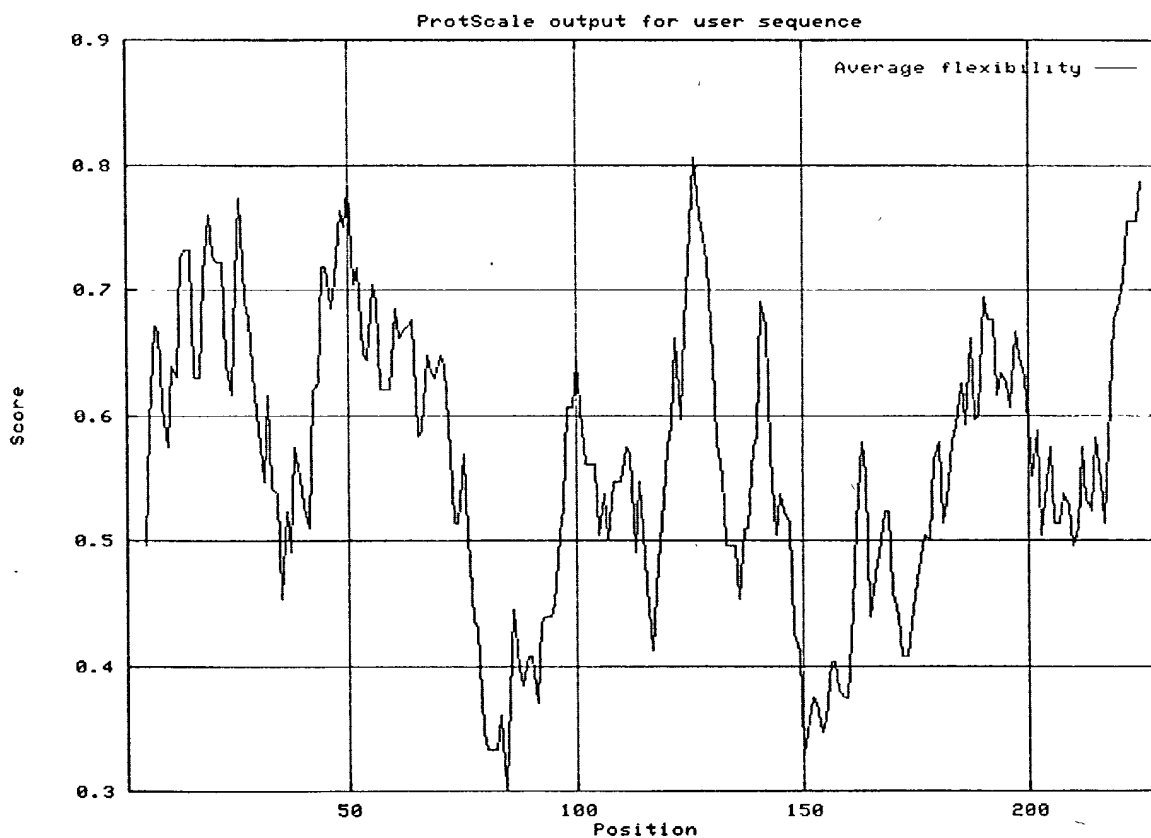


Figure 9: 85P1B3 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

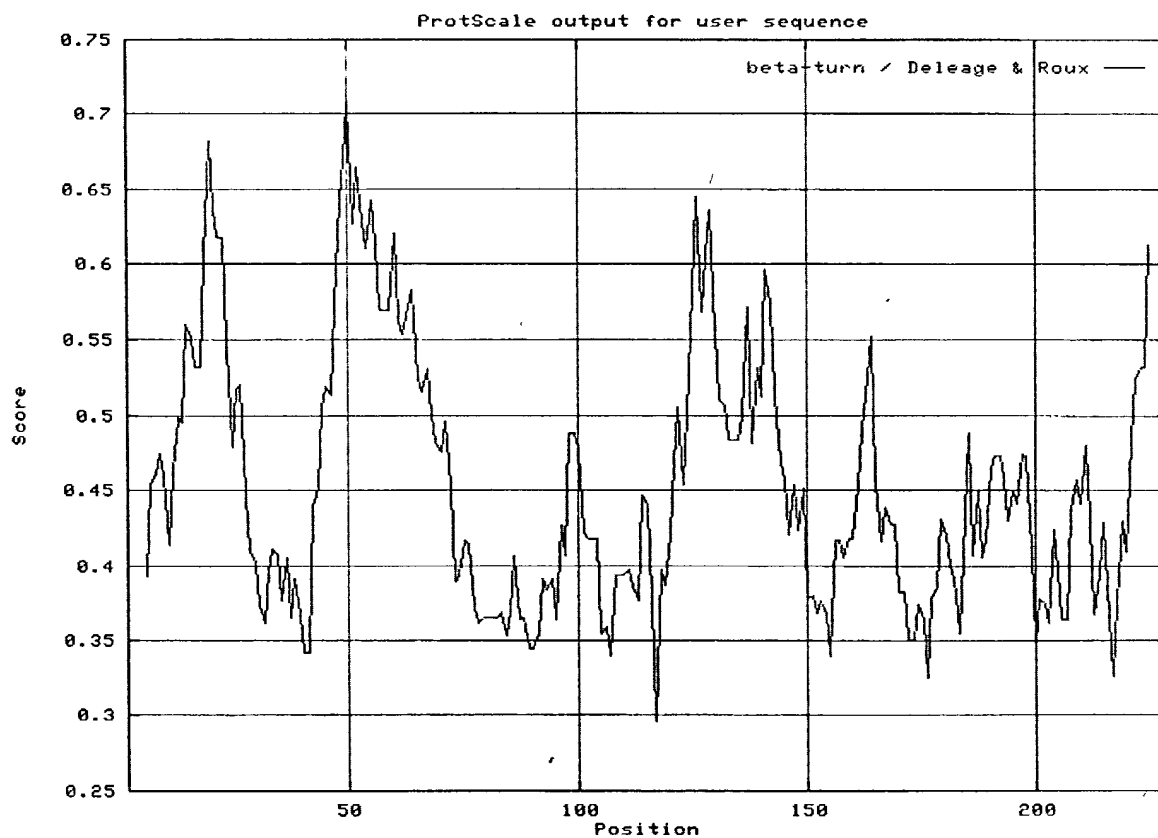


Figure 10 RT-PCR analysis of 85P1B3 expression.

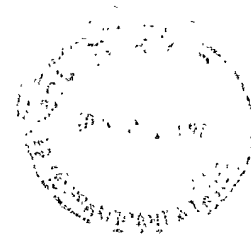
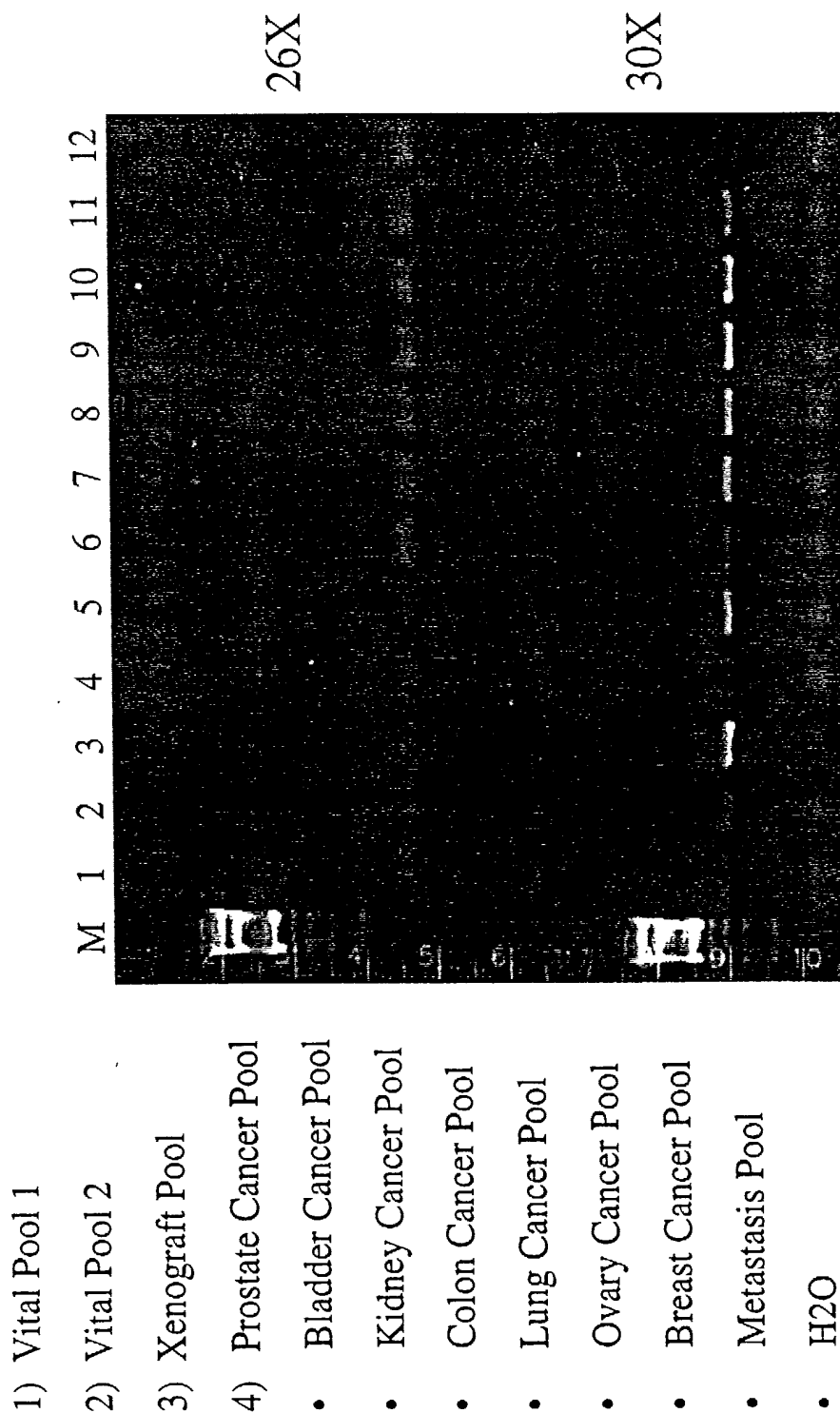


Figure 11 Expression of 85P1B3 in Normal Human Tissues

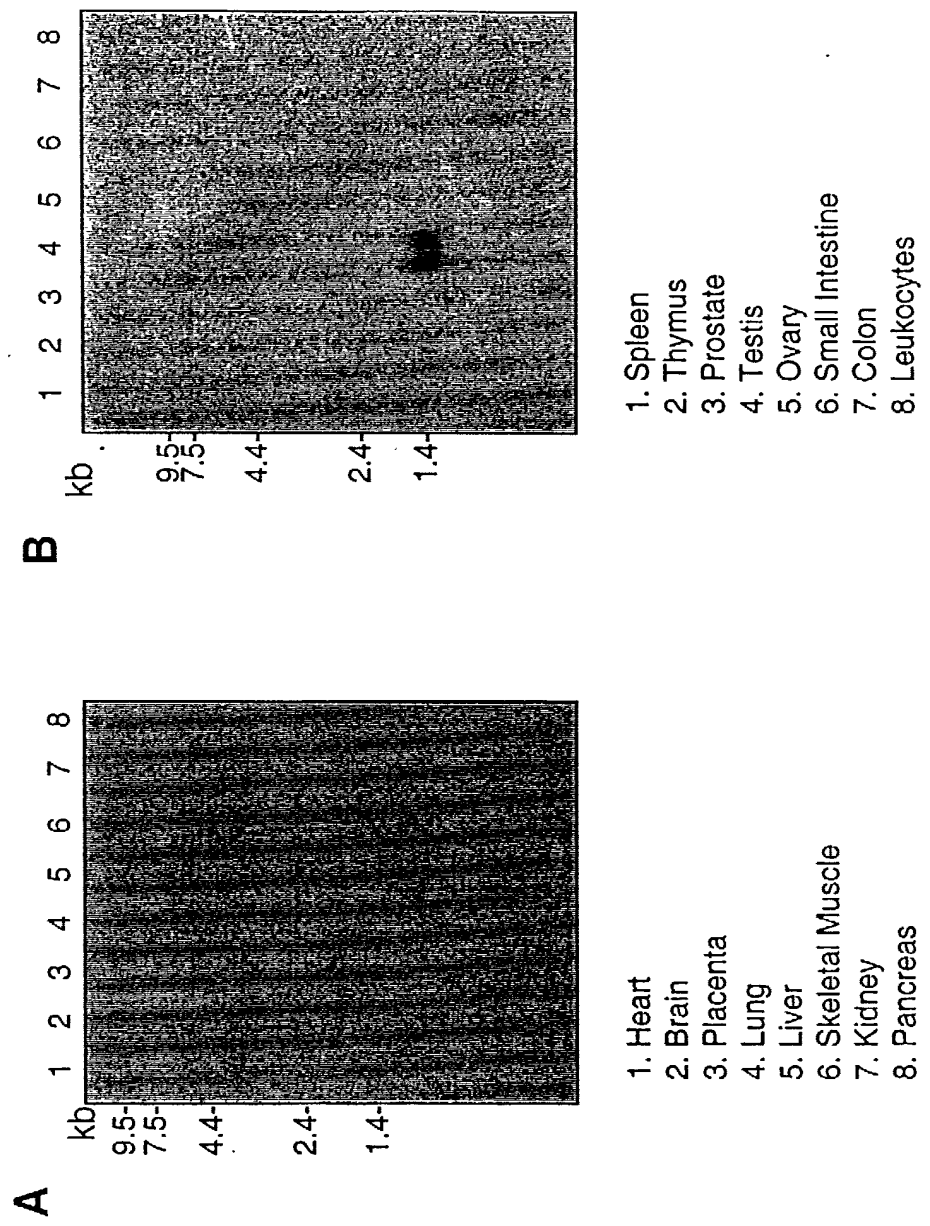


Figure 12 Expression of 85P1B3 in Human Cancer Cell lines

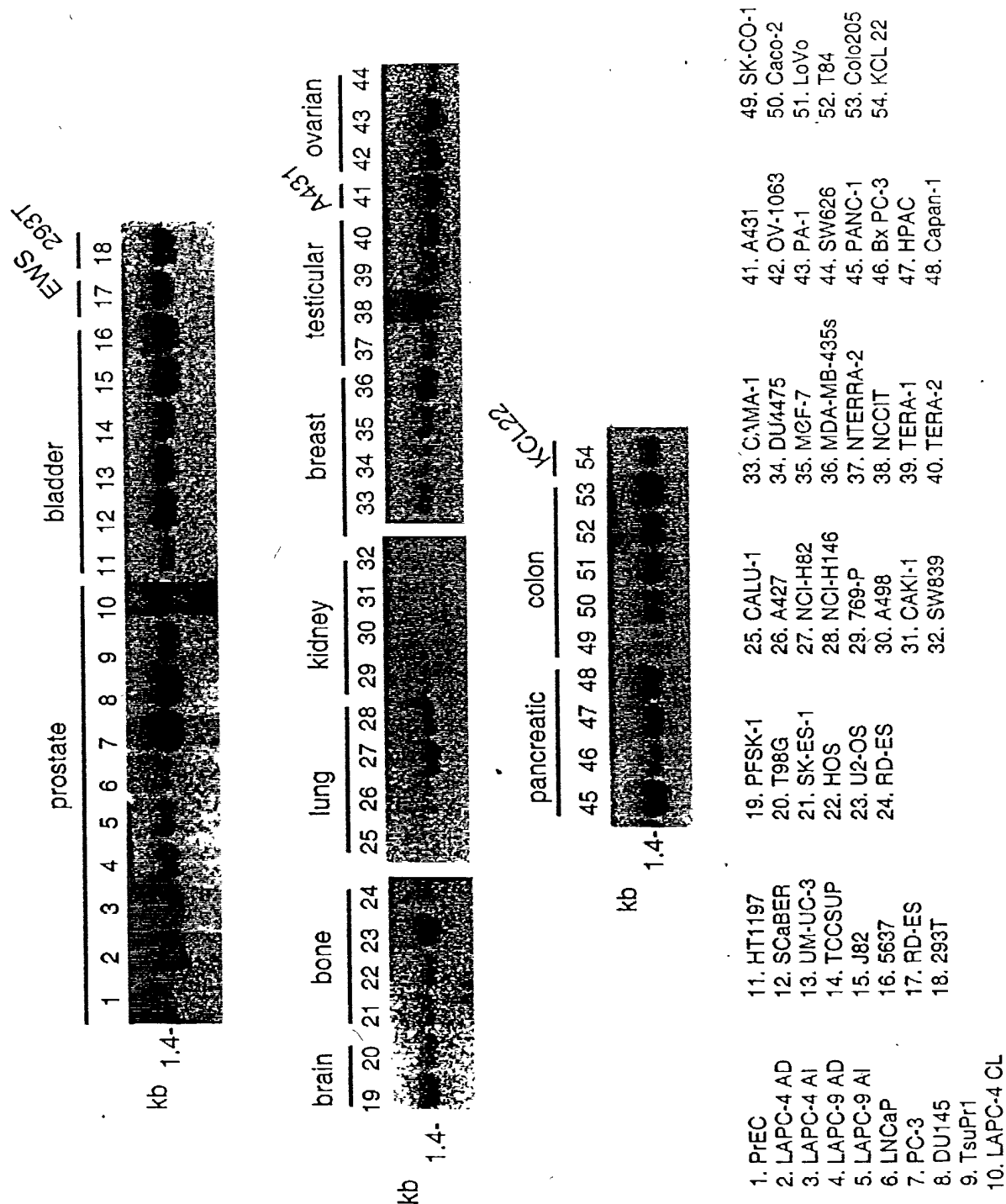
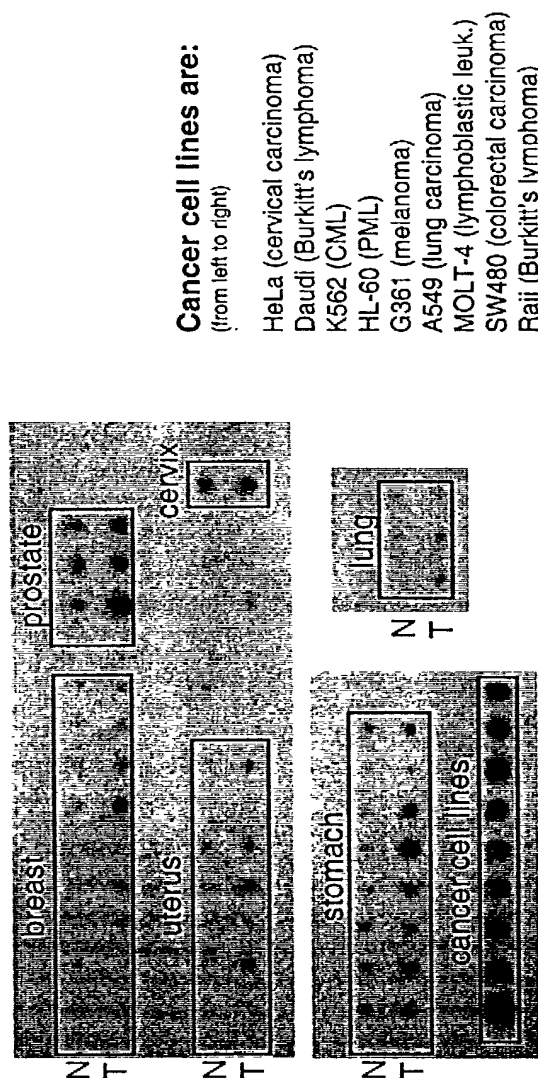
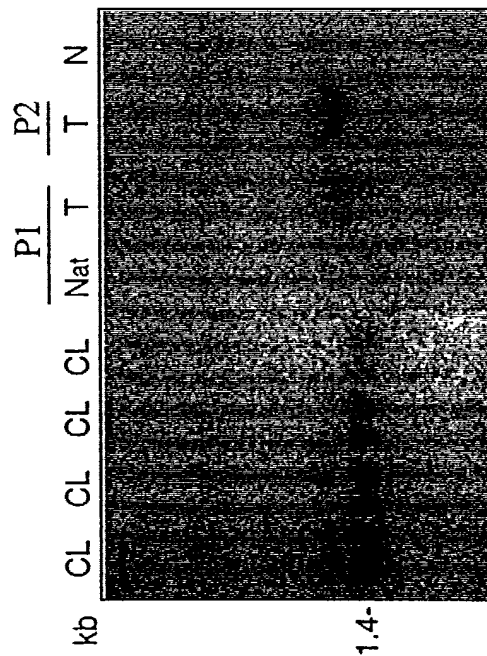


Figure 13 Expression of 85P1B3 in Patient Cancer Specimens and Cancer Cell Lines



T = tumor RNA
N = normal adjacent tissue RNA

Figure 14 Expression of 85P1B3 in Colon Cancer Patient Specimens

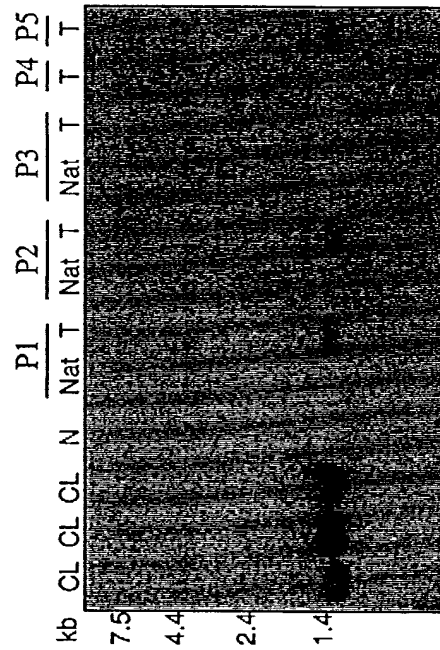


Cell Lines (CL) - Colo 205, LoVo, T84, Caco-2
 N = Normal Colon
 Nat = Normal Adjacent tissue
 T = Tumor

P1 - Stage III, T2N1MX
 P2 - Stage III, T3N1MX

00947052 . 042602

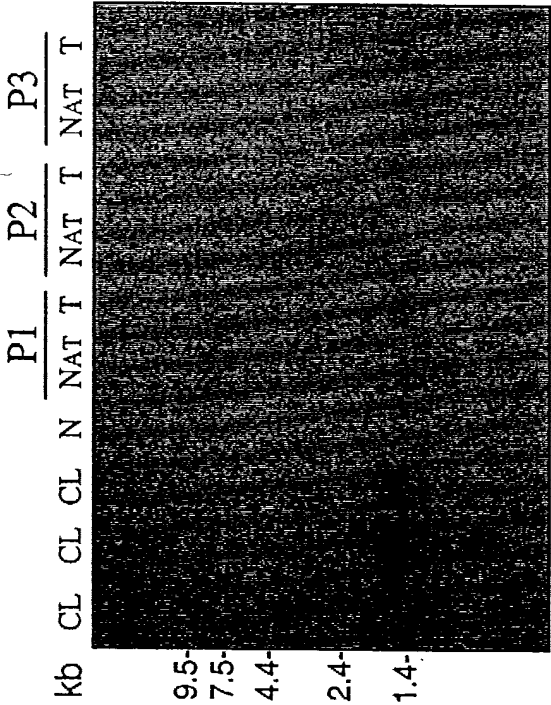
Figure 15 Expression of 85P1B3 in Bladder Cancer Patient Specimens



P1 - Transitional, grade 2
P2 - Transitional, grade 3/2
P3 - Transitional
P4 - Polypoid cystitis
P5 - Papillary, grade 3

CL = cell lines listed in order: UM-UC-3, J82, SCABER
P = Patient
N = Normal Bladder
Nat = Normal adjacent tumor
T = Tumor

Figure 16 Expression of 85P1B3 in Lung Cancer Patient Specimens



P1 - Squamous, stage IB
P2 - Squamous, stage IIB
P3 - Squamous, stage IIIA

CL = cell lines (listed in order):
A427, NCI-H82, NCI-H146

P = Patient
N = Normal Lung
NAT = Normal adjacent tissue
T = Tumor

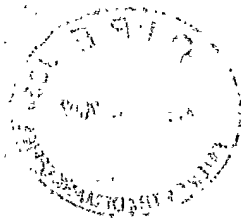
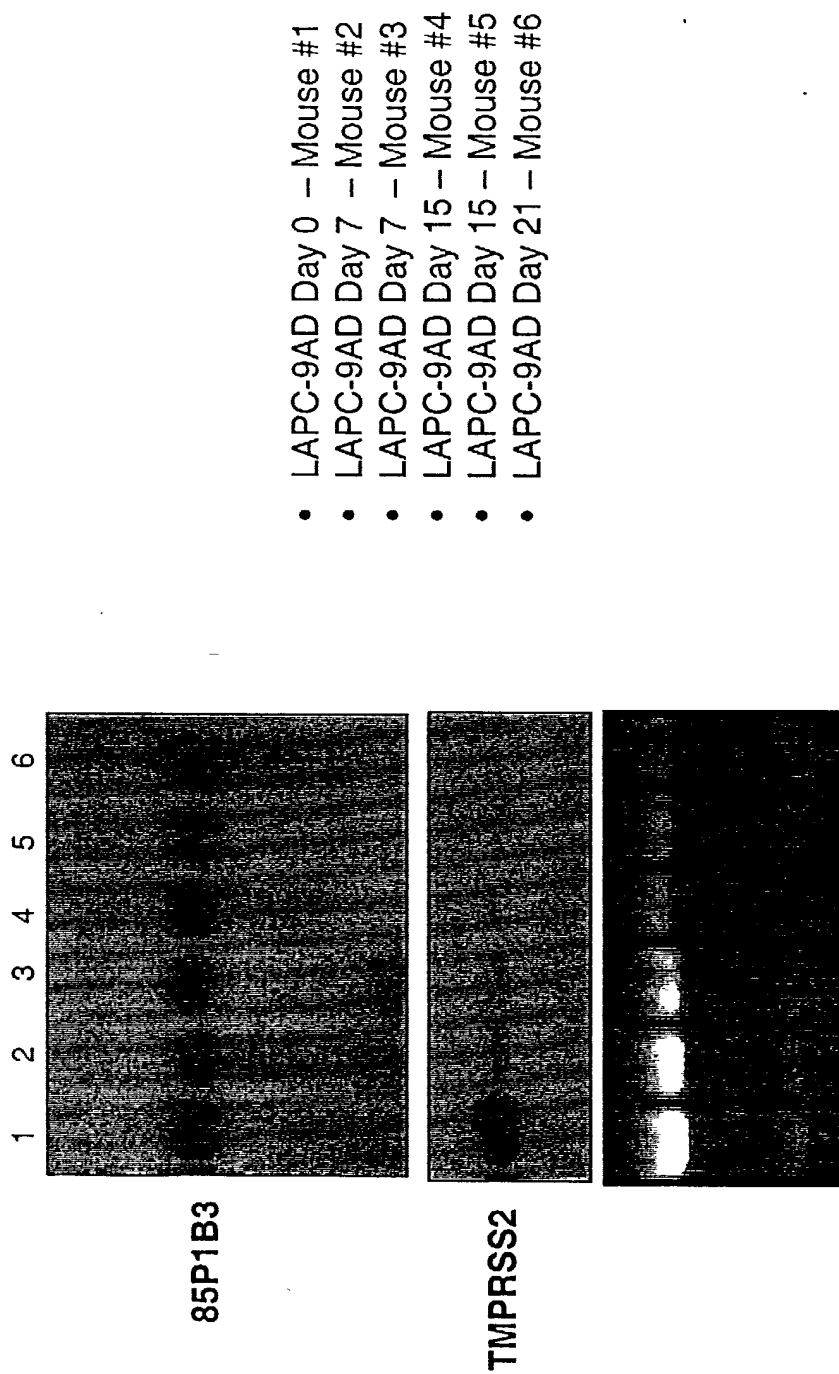
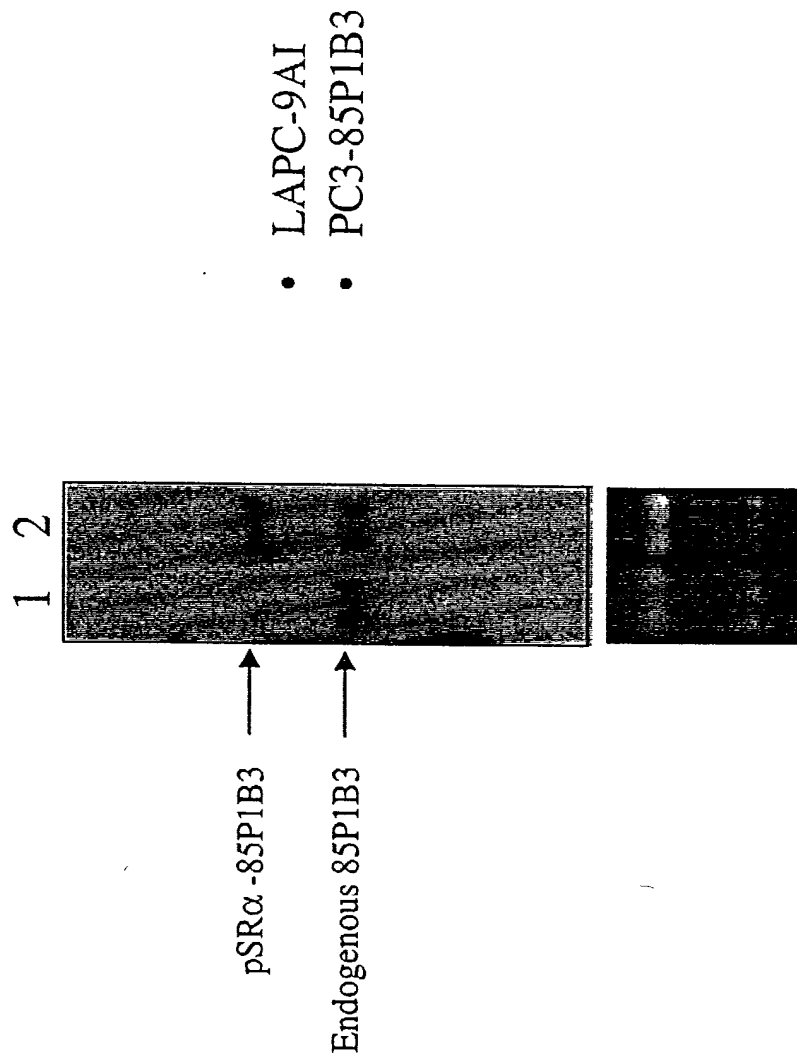


Figure 17 Expression of 85P1B3 in Prostate Cancer Xenografts Following Castration



- LAPC-9AD Day 0 – Mouse #1
- LAPC-9AD Day 7 – Mouse #2
- LAPC-9AD Day 7 – Mouse #3
- LAPC-9AD Day 15 – Mouse #4
- LAPC-9AD Day 15 – Mouse #5
- LAPC-9AD Day 21 – Mouse #6

Figure 18 Expression of 85P1B3 in PC3 Cells Following Retroviral-Mediated Gene Delivery



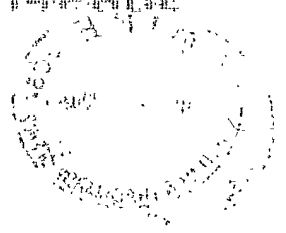
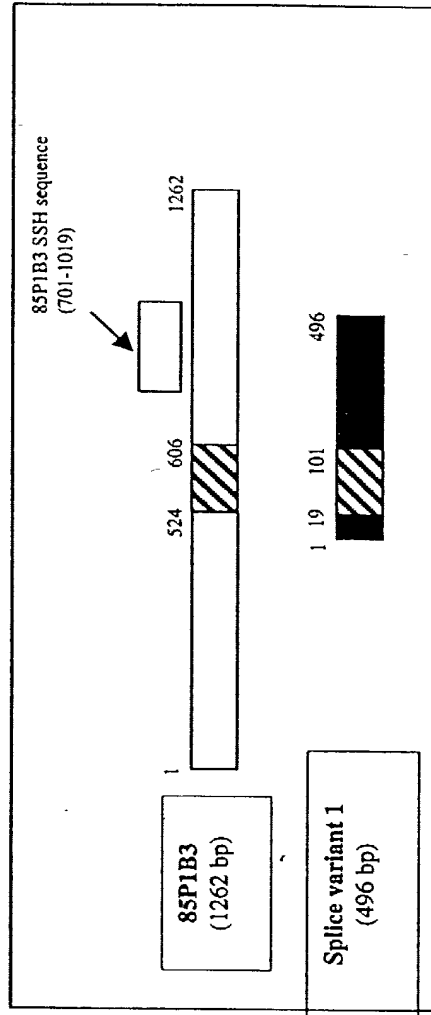
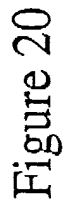


Figure 19.





MAAQLRHRRCATTPRGDFCGGTERAIDQASFTTSMEDTQVVGSSPLGPAGLGAEEPAAGPQLPSWL
 ccc
 QPERCAVFQCAQCHAVLADSVHLAWDLGRSLGAWFSRVTVNNVLEAPFLVGIEGSLKSTYNLLFCGSC
 chhh
 GIPVGFHLYSTHAALAAALRGHFCLSSDKMVCYLLKTKAIVNASMDIQNVPLSEKIAELXKIVLTHNRL
 cccchhh
 KSLMKILSEVTPDQSKPEN (SEQ ID NO:729)
 hhhhhhhccccccccccc

(Musical notation)

No transmembrane domains, soluble protein